CLAIMS

1. A method for the prediction of response to cancer treatment, by the detection of at least 2 markers characterized in that the markers are genes and fragments thereof or genomic nucleic acid sequences that are located on one chromosomal region which is altered in malignant neoplasia.

2. The method of claim 1 wherein the treatment is an antibody treatment, antihormonal treatment, anti-growth factor treatment, taxol based treatment, anthracyclin based treatment and platinum salt based treatment.

3. The method of claim 1 wherein the treatment includes Herceptin™, trastuzumab or 2C4 antibodies.

4. The method of claim 1 characterized in that the markers are:

a) genes that are located on one or more chromosomal region(s) which is/are altered in malignant neoplasia; and

b)

i) receptor and ligand; or
ii) members of the same signal transduction pathway; or
iii) members of synergistic signal transduction pathways; or
iv) members of antagonistic signal transduction pathways; or
v) transcription factor and transcription factor binding site; or
vi) integral parts of heteromeric complexes

5. The method of claim 1 or 2 wherein the malignant neoplasia is breast cancer, ovarian cancer, gastric cancer, colon cancer, esophageal cancer, mesenchymal cancer, bladder cancer or non-small cell lung cancer.

6. The method of any of claims 1 to 5 wherein at least one chromosomal region is defined as the cytogenetic region: 1p13, 1q32, 3p21-p24, 5p13-p14, 8q23-q24, 11q13, 12q13,17q12-q24, 17q11.2-21.3 or 20q13.

7. A method for the prediction, diagnosis or prognosis of malignant neoplasia by the detection of at least one marker characterized in that the marker is selected from:

a) a polynucleotide or polynucleotide analog comprising at least one of the sequences of SEQ ID NO: **319 to 389;**

b) a polynucleotide or polynucleotide analog which hybridizes under stringent conditions to a polynucleotide specified in (a) and encodes a polypeptide exhibiting the same biological function as specified for the respective sequence in Table 2 or 3

c) a polynucleotide or polynucleotide analog the sequence of which deviates from the polynucleotide specified in (a) and (c) due to the generation of the genetic code encoding a polypeptide exhibiting the same biological function as specified for the respective sequence in Table 2 or 3

d) a polynucleotide or polynucleotide analog which represents a specific fragment, derivative or allelic variation of a polynucleotide sequence specified in (a) to (d)

e) a purified polypeptide encoded by a polynucleotide or polynucleotide analog sequence specified in (a) to (e)

f) e purified polypeptide comprising at least one of the sequences of SEQ ID NO: 397 - 467;

Are detected.

8. The method according to any of claims 1 to 6 wherein the markers are selected from:

a) a polynucleotide or polynucleotide analog comprising at least one of the sequences of SEQ ID NO: 2 to 6, 8, 9, 11 to 16, 18, 19, 21 to 26, 53 to 76 or 315 to 389

b) a polynucleotide or polynucleotide analog which hybridizes under stringent conditions to a polynucleotide specified in (a) and encodes a polypeptide exhibiting the same biological function as specified for the respective sequence in Table 2 or 3

c) a polynucleotide or polynucleotide analog the sequence of which deviates from the polynucleotide specified in (a) and (b) due to the generation of the genetic code encoding a polypeptide exhibiting the same biological function as specified for the respective sequence in Table 2 or 3

d) a polynucleotide or polynucleotide analog which represents a specific fragment, derivative or allelic variation of a polynucleotide sequence specified in (a) to (c)

e) a purified polypeptide encoded by a polynucleotide sequence or polynucleotide analog specified in (a) to (d)

f) A purified polypeptide comprising at least one of the sequences of SEQ ID NO: 27 to 52 or 76 to 98 or 393 to 467

are detected.

9. A diagnostic kit for conducting the method of claims 1 to 8.